

CLAIMS

We claim:

1. A method for detecting, or for detecting and distinguishing between or among colon cell proliferative disorders in a subject, comprising contacting genomic DNA obtained from the subject with at least one reagent, or series of reagents that distinguishes between methylated and non-methylated CpG dinucleotides within at least one target region of the genomic DNA, wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:58, and complements thereof, wherein said contiguous nucleotides comprise at least one CpG dinucleotide sequence, and whereby detecting, or detecting and distinguishing between or among colon cell proliferative disorders is, at least in part, afforded.
2. The method of claim 1, wherein colorectal carcinoma is distinguished from at least one condition selected from the group consisting of colon adenoma, normal colon tissue, non-colon tissues and non-colon cell proliferative disorders.
3. The method of claim 1, wherein colon adenoma is distinguished from at least one condition selected from the group consisting of colon carcinoma, normal colon tissue, non-colon tissues and non-colon cell proliferative disorders.
4. The method of claim 1, wherein at least one of colorectal carcinoma tissue or colon adenomas is distinguished from at least one tissue selected from the group consisting of colon polyps less than 1cm in diameter, inflammatory colon tissue, and normal colon tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1-12, 15-20, 22, 25-36, 38-49, 51-58, and complements thereof.
5. The method of claim 1, wherein colorectal carcinoma is distinguished from at least one tissue selected from the group consisting of non-colon healthy tissue, peripheral blood lymphocytes and non-colon cancer tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous

- nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1-23, 26-36, 38-43, 45-49, 51-58 and complements thereof.
6. The method of claim 1, wherein colorectal carcinoma is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue, normal colon tissue, non-colon healthy tissue, peripheral blood lymphocytes, colon adenomas and non-colon cancer tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1-3, 5-13, 15-23, 26-36, 38-43, 45-49, 51-58, and complements thereof.
 7. The method of claim 1, wherein colorectal carcinoma is distinguished from colon adenomas, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:11, 25, 27, 38, 40, 45, 53, and complements thereof.
 8. The method of claim 1, wherein at least one of colorectal carcinoma tissue, or large adenomas is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue, and normal colon tissue.
 9. The method of claim 1, wherein colorectal carcinoma tissue is distinguished from at least one of inflammatory colon tissue and normal colon tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1-3, 5-23, 25-36, 38-49, 51-58, and complements thereof.
 10. The method of claim 1, wherein at least one of colorectal carcinoma tissue, or colon adenomas is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue, normal colon tissue, non-colon healthy tissue, peripheral blood lymphocytes, and non-colon cancer tissue, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1-36, 38-43, 45-58, and complements thereof.

11. The method of claim 1, wherein tissues originating from the colon are distinguished from tissues of non-colon origin.
12. The method of claim 1, wherein cell proliferative disorders are distinguished from healthy tissues, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1-36, 38-43, 45-49, 51-58, and complements thereof.
13. A method for detecting, or for detecting and distinguishing between or among colon cell proliferative disorders in a subject, comprising:
 - obtaining, from a subject, a biological sample having subject genomic DNA;
 - contacting the genomic DNA, or a fragment thereof, with one reagent or a plurality of reagents that distinguishes between methylated and non methylated CpG dinucleotide sequences within at least one target sequence of the genomic DNA, or fragment thereof, wherein the target sequence comprises, or hybridizes under stringent conditions to, at least 16 contiguous nucleotides of a sequence taken from the group consisting of SEQ ID NO:1 to SEQ ID NO:58, and complements thereof, said contiguous nucleotides comprising at least one CpG dinucleotide sequence; and
 - determining, based at least in part on said distinguishing, the methylation state of at least one target CpG dinucleotide sequence, or an average, or a value reflecting an average methylation state of a plurality of target CpG dinucleotide sequences, whereby detecting, or detecting and distinguishing between or among colon cell proliferative disorders is, at least in part, afforded.
14. The method of claim 13, wherein detecting, or detecting and distinguishing between or among colon cell proliferative disorders comprises detecting, or detecting and distinguishing between or among one or more tissues selected from the group consisting of colorectal carcinoma, colon adenoma, inflammatory colon tissue, grade 2 dysplasia colon adenomas less than 1 cm in diameter, grade 3 dysplasia colon adenomas larger than 1 cm in diameter, normal colon tissue, non-colon normal tissue, body fluids and non-colon cancer tissue.

15. The method of claim 13, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises converting unmethylated cytosine bases within the target sequence to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties.
16. The method of claim 13, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence(s) comprises methylation state-dependent conversion or non-conversion of at least one CpG dinucleotide sequence to the corresponding converted or non-converted dinucleotide sequence within a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and contiguous regions thereof corresponding to the target sequence.
17. The method of claim 13, wherein the biological sample is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.
18. The method of claim 13, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises use of at least one nucleic acid molecule or peptide nucleic acid (PNA) molecule comprising, in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof.
19. The method of claim 18, wherein the contiguous sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.
20. The method of claim 18, comprising use of at least two such nucleic acid molecules, or peptide nucleic acid (PNA) molecules.
21. The method of claim 18, comprising use of at least two such nucleic acid molecules as primer oligonucleotides for the amplification of a sequence selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:58, SEQ ID NO: 304 to SEQ ID NO:535,

sequences complementary thereto, and regions thereof that comprise or hybridize under stringent conditions to the primers.

22. The method of claim 18, comprising use of at least four such nucleic acid molecules, peptide nucleic acid (PNA) molecules.

23. A method for detecting, or detecting and distinguishing between or among colon cell proliferative disorders in a subject, comprising:

a) obtaining, from a subject, a biological sample having subject genomic DNA;

b) extracting or otherwise isolating the genomic DNA;

c) treating the genomic DNA of b), or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties;

d) contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence of at least 9 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof, wherein the treated genomic DNA or the fragment thereof is either amplified to produce at least one amplificate, or is not amplified; and

e) determining, based on a presence or absence of, or on a property of said amplificate, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting SEQ ID NO:1 to SEQ ID NO:58, or an average, or a value reflecting an average methylation state of a plurality of said CpG dinucleotides, whereby at least one of detecting, or detecting and distinguishing between colon cell proliferative disorders is, at least in part, afforded.

24. The method of claim 23, wherein treating the genomic DNA, or the fragment thereof in c), comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof.

25. The method of claim 23, wherein contacting or amplifying in d) comprises use of at least one method selected from the group consisting of: use of a heat-resistant DNA

- polymerase as the amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); generation of a amplificate nucleic acid molecule carrying a detectable labels; and combinations thereof.
26. The method of claim 25, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.
27. The method of claim 23, wherein the biological sample obtained from the subject is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.
28. The method of claim 23, wherein colorectal carcinoma is distinguished from at least one condition selected form the group consisting of colon adenoma, inflammatory colon tissue, colon adenomas with grade 2 dysplasia less than 1 cm in diameter, colon adenomas with grade 3 dysplasia equal to or greater than 1 cm in diameter, normal colon tissues, non-colon normal tissue, body fluids, and non-colon cancer tissue.
29. The method of claim 23, further comprising in step d) the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized.
30. The method of claim 29, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case modified at the 5'-end thereof to preclude degradation by an enzyme having 5'-3' exonuclease activity.

31. The method of claim 29, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case lacking a 3' hydroxyl group.
32. The method of claim 29, wherein the amplification enzyme is a polymerase lacking 5'-3' exonuclease activity.
33. The method of claim 23, wherein determining in e) comprises hybridization of at least one nucleic acid molecule or peptide nucleic acid molecule in each case comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof.
34. The method of claim 33, wherein said nucleic acid corresponds to a sequence selected from the group consisting of SEQ ID NOS: SEQ ID NOS: 1162, 1163, 1201, 1202, 1208, 1211, 1217, 1274, 1288, 1275, 1289, 1299, 1308, 1309, 1341, 1342, 1347, 1351, 1354, 1372, 1423, 1424, 1425, 1427, 1432, 1433, 1434, 1435, 1436, 1437, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1370, 1371, 1400, 1450, 1461, 1451, 1462, 1467, 1470, 1473, 1475, 1535, 1536, 1542, 1544, 1569, 1570, 1583, 1590, 1595, 1666, 1704, 1596, 1601, 1603, 1667, 1705, 1722, 1723, 1727, 1735, 1746, 1747, 1768, 1769, 1773, 1803, 1804, 1807, 1810, 1832, 1833, 1836, 1867, 1871, 1901, 1902, 1908, 1911, 1924, 1925, 1937, 1938, 1943, 1946, 1949, 1956, 1957, 1978, 1979, 1986, 1992, 1998, 2001, 2003, 2010, 2020, 2025, 2029, 2030, 2113, 2163, 2201, 2209, 2231, 2259, 2304, 2326, 2338, 2348, 2351, 2369, 2407, 2471, 2488, 2557, 2584, 2602, 2616, 2657, 2661, 2664, 2671, 2683, 2709, 2753, 2756, 2758, 2761, 2766, 2770, 2774, 2778, 2799, 2807, 2813, 2819, 2822, 2826, 2848, 2857, 2900, 2906, 2908, 2910, 2913, 2921, 2925, 2940, 2943, 2952, 2964, 2983, 2986, 3009, 3012, 3015, 3024, 3030, 3035, 3046, 3058, 3062, 3067, 3070, 3074, 3077, 3079, 3082, 3087, 3095, 3099, 3102, 3106, 3112, 3120, 3125, 3129, 3132, 3141, 3143, 3154, 3156, 3158, 3161, 3177, 3188, 3191, 3193, 3200, 3208, 3211, 3220, 3231, 3241, 3251, 3254, 3258, 3263, 3272, 3277, 3288, 3294, 3296, 3299, 3303, 3317, 3323, 3326, 3329, 3336, 3341, 3362, 3366, 3370, 3375, 3379, 3382, 3387, 3394, 3398, 3405, 3407, 3410, 3412, 3416, 3422, 3425, 3430, 3449, 3451, 3457, 3460, 3465,

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35. The method of claim 33, wherein at least one such hybridizing nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase.
36. The method of claim 33, wherein a plurality of such hybridizing nucleic acid molecules or peptide nucleic acid molecules are bound to a solid phase in the form of a nucleic acid or peptide nucleic acid array selected from the array group consisting of linear or substantially so, hexagonal or substantially so, rectangular or substantially so, and combinations thereof.
37. The method of claim 33, further comprising extending at least one such hybridized nucleic acid molecule by at least one nucleotide base.
38. The method of claim 23, wherein determining in e), comprises sequencing of the amplificate.
39. The method of claim 23, wherein contacting or amplifying in d), comprises use of methylation-specific primers.
40. The method of claim 39 wherein the sequence of said methylation specific primers is taken from the group consisting of SEQ ID NOS:2754, 2757, 2759, 2767, 2768, 2772, 2776, 2779, 2784, 2785, 2786, 2789, 2791, 2792, 2794, 2797, 2798, 2801, 2805, 2806,

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41. The method of claim 23 comprising in d) using primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides; and further comprising in e) the use of

at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing in e) of the amplificate.

42. The method of claim 23 comprising in d) use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized; and further comprising in e) the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under

moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing in e) of the amplificate.

43. The method of claim 23, comprising in d) amplification by primer oligonucleotides comprising one or more CpG, TpG or CpA dinucleotides and further comprising in e) hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535.
44. The method of claim 23, comprising in d) the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized, and further comprising in e) hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535.
45. The method according to any one of claims 41 and 43, wherein the primer oligonucleotides of d) are selected from the group consisting of SEQ ID NOS:2754, 2757, 2759, 2767, 2768, 2772, 2776, 2779, 2784, 2785, 2786, 2789, 2791, 2792, 2794, 2797, 2798, 2801, 2805, 2806, 2809, 2811, 2815, 2817, 2824, 2830, 2832, 2833, 2834,

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46. The method according to any one of claims 42 and 44, wherein the nucleic acid molecule or peptide nucleic acid molecule of d) are selected from the group consisting of SEQ ID NOS: 2114, 2119, 2124, 2125, 2127, 2132, 2133, 2135, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2031, 2082, 2087, 2089, 2094, 2095, 2096, 2097, 2099, 2107, 1980, 2018, 2022, 2023, 2026, 1939, 1966, 1973, 1974, 1975, 1926, 1930, 1931, 1932, 1933, 1934, 1903, 1917, 1921, 1834, 1896, 1805, 1819, 1821, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1770, 1782, 1785, 1786, 1788, 1789, 1790, 1792, 1795, 1796, 1797, 1798, 1799, 1800, 1748, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1724, 1741, 1597, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1633, 1634, 1635,

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1217, 1274, 1288, 1275, 1289, 1299, 1308, 1309, 1341, 1342, 1347, 1351, 1354, 1372, 1423, 1424, 1425, 1427, 1432, 1433, 1434, 1435, 1436, 1437, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1370, 1371, 1400, 1450, 1461, 1451, 1462, 1467, 1470, 1473, 1475, 1535, 1536, 1542, 1544, 1569, 1570, 1583, 1590, 1595, 1666, 1704, 1596, 1601, 1603, 1667, 1705, 1722, 1723, 1727, 1735, 1746, 1747, 1768, 1769, 1773, 1803, 1804, 1807, 1810, 1832, 1833, 1836, 1867, 1871, 1901, 1902, 1908, 1911, 1924, 1925, 1937, 1938, 1943, 1946, 1949, 1956, 1957, 1978, 1979, 1986, 1992, 1998, 2001, 2003, 2010, 2020, 2025, 2029, 2030, 2113, 2163, 2201, 2209, 2231, 2259, 2304, 2326, 2338, 2348, 2351, 2369, 2407, 2471, 2488, 2557, 2584, 2602, 2616, 2657, 2661, 2664, 2671, 2683, 2709 and SEQ ID NO:2724.

47. A method for detecting, or for detecting and distinguishing between or among colon cell proliferative disorders in a subject, comprising:

a) obtaining, from a subject, a biological sample having subject genomic DNA;

b) extracting, or otherwise isolating the genomic DNA;

c) contacting the genomic DNA of b), or a fragment thereof, comprising at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:58, and sequences that hybridize under stringent conditions thereto, with one or more methylation-sensitive restriction enzymes, wherein the genomic DNA is, with respect to each cleavage recognition motif thereof, either cleaved thereby to produce cleavage fragments, or not cleaved thereby; and

d) determining, based on a presence or absence of, or on property of at least one such cleavage fragment, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:58, or an average, or a value reflecting an average methylation state of a plurality of said CpG dinucleotides, whereby at least one of detecting, or of detecting and differentiating between or among colon cell proliferative disorders is, at least in part, afforded.

48. The method of claim 47, further comprising, prior to determining in d), amplifying of the digested or undigested genomic DNA.

49. The method of claim 48, wherein amplifying comprises use of at least one method selected from the group consisting of: use of a heat resistant DNA polymerase as an amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); generation of a amplificate nucleic acid carrying a detectable label; and combinations thereof.
50. The method of claim 49, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.
51. The method of claim 47, wherein the biological sample obtained from the subject is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.
52. An isolated treated nucleic acid derived from genomic SEQ ID NO:1 to SEQ ID NO:58, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.
53. A nucleic acid, comprising at least 16 contiguous nucleotides of a treated genomic DNA sequence selected from the group consisting of SEQ ID NO:304 to SEQ ID NO:535, and sequences complementary thereto, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.
54. The nucleic acid of any one of claims 52 and 53, wherein the contiguous base sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.
55. The nucleic acid of any one of claims 52 and 53, wherein the treatment comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof.

56. An oligomer, comprising a sequence of at least 9 contiguous nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a treated genomic DNA sequence selected from the group consisting of SEQ ID NOS:304-534, and SEQ ID NO:535.
57. The oligomer of Claim 56, comprising at least one CpG , CpA or TpG dinucleotide sequence.
58. The oligomer of claim 57, having a sequence selected from the group consisting of SEQ ID NOS:674-1158, and SEQ ID NO:1159.
59. A set of oligomers, comprising at least two oligonucleotides according, in each case, to any one of Claims 56 through 58.
60. A set of isolated nucleic acids, comprising at least two oligomers corresponding to sequences selected from the group consisting of SEQ ID NOS:59-302, and SEQ ID NO:303.
61. A set of isolated nucleic acids, comprising at least two oligomers having, in each case, at least 9 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:59-302, and SEQ ID NO:303.
62. The use of a set of oligonucleotides according to any one of claims 59, 60 or 61 for at least one of: detection of; detection and differentiation between or among subclasses of; diagnosis of; prognosis of; treatment of; monitoring of; and treatment and monitoring of colon cell proliferative disorders.
63. The use of a nucleic acid according to any one of claims 52 through 55, an oligonucleotide according to any one of claims 56 through 58, or a set of oligonucleotides according to any one of claims 59, 60 or 61 for detecting, or detecting and distinguishing between or among colon cell proliferative disorders comprises detecting, or detecting and distinguishing between or among one or more tissues selected from the group consisting of colorectal carcinoma, colon adenoma, inflammatory colon tissue, grade 2 dysplasia colon adenomas less than 1 cm in diameter, grade 3 dysplasia colon adenomas larger than 1 cm in diameter, normal colon tissue, non-colon healthy tissue and non-colon cancer tissue.

64. The set of nucleic acids of Claim 61, comprising at least two oligomers selected from one of the oligomer subgroups consisting of: SEQ ID NOS:59-285; SEQ ID NOS:59-109, 113-223, 227-293; SEQ ID NOS:59-109, 113-161, 164-223, 227-285, 287-293; SEQ ID NOS:89, 90, 126-135, 147-151, 224-226, 253-256, 261-267, 283-285; SEQ ID NOS:59-161, 164-293; SEQ ID NOS:59-109, 113-299; and SEQ ID NOS:59-109, 113-293, and SEQ ID NOS:296-299.
65. The set of nucleic acids of Claim 58, comprising at least two oligomers selected from one of the oligomer subgroups consisting of: SEQ ID NOS:681 - 683, 683, 684, 684, 685, 685, 686, 686, 687, 687, 688, 688 - 691, 691, 692, 692 - 695, 695, 696, 696 - 699, 699, 700, 700 - 709, 709, 710, 710 - 725, 725, 726, 726, 727, 727, 728, 728 - 760, 760, 761, 761, 762, 762, 763, 763 - 784, 784, 785, 785, 786, 786, 787, 787 - 802, 802, 803, 803 - 814, 814, 815, 815 - 832, 832, 833, 833 - 836, 836, 837, 837 - 872, 872, 873, 873 - 876, 876, 877, 877, 878, 878, 879, 879 - 882, 882, 883, 883 - 892, 892, 893, 893 - 896, 896, 897, 897 - 909, 909, 910, 910, 911, 911, 912, 912 - 915, 915, 916, 916 - 921, 921 - 925, 925, 926, 926 - 939, 939, 940, 940, 941, 941, 942, 942 - 944, 944 - 957, 957, 958, 958, 959, 959, 960, 960, 961, 961, 962, 962 - 971, 971, 972, 972, 973, 973, 974, 974, 975, 975, 976, 976 - 979, 979, 980, 980, 981, 981 - 988, 988, 989, 989 - 994, 994, 995, 995 - 998, 998, 999, 999, 1000, 1000, 1001, 1001, 1002, 1002, 1003, 1003 - 1006, 1006, 1007, 1007 - 1016, 1016, 1017, 1017, 1018, 1018, 1019, 1019 - 1028, 1028, 1029, 1029 - 1034, 1034, 1035, 1035 - 1046, 1046, 1047, 1047 - 1058, 1058, 1059, 1059, 1060, 1060, 1061, 1061, 1062, 1062, 1063, 1063 - 1070, 1070, 1071, 1071, 1072, 1072, 1073, 1073, 1074, 1074, 1075, 1075 - 1078, 1078, 1079, 1079 - 1084, 1084, 1085, 1085, 1086, 1086, 1087, 1087 - 1092, 1092, 1093, 1093, 1094, 1094, 1095, 1095 - 1102, 1102, 1103, 1103 - 1114, 1114, 1115, 1115 - 1119, 1119, 1120, 1120 - 1124; SEQ ID NOS:681 - 683, 683, 684, 684, 685, 685, 686, 686, 687, 687, 688, 688 - 691, 691, 692, 692 - 695, 695, 696, 696 - 699, 699, 700, 700 - 709, 709, 710, 710 - 725, 725, 726, 726, 727, 727, 728, 728 - 760, 760, 761, 761, 762, 762, 763, 763 - 777, 784, 784, 785, 785, 786, 786, 787, 787 - 802, 802, 803, 803 - 814, 814, 815, 815 - 832, 832, 833, 833 - 836, 836, 837, 837 - 872, 872, 873, 873 - 876, 876,

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66. The use of any one of claims 62 or 63, wherein at least one of colorectal carcinoma tissue or colon adenomas is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue and normal colon tissue, and wherein the set of nucleic acids comprises at least two oligomers selected from one of the oligomer groups consisting of: SEQ ID NOS:59 - 285; and SEQ ID NOS:681 - 683, 683, 684, 684, 685, 685, 686, 686, 687, 687, 688, 688 - 691, 691, 692, 692 - 695, 695, 696, 696 - 699, 699, 700, 700 - 709, 709, 710, 710 - 725, 725, 726, 726, 727, 727, 728, 728 - 760, 760, 761, 761, 762, 762, 763, 763 - 784, 784, 785, 785, 786, 786, 787, 787 - 802, 802, 803, 803 - 814, 814, 815, 815 - 832, 832, 833, 833 - 836, 836, 837, 837 - 872, 872, 873, 873 - 876, 876, 877, 877, 878, 878, 879, 879 - 882, 882, 883, 883 - 892, 892, 893, 893 - 896, 896, 897, 897 - 909, 909, 910, 910, 911, 911, 912, 912 - 915, 915, 916, 916 - 921, 921 - 925, 925, 926, 926 - 939, 939, 940, 940, 941, 941, 942, 942 -

944, 944 - 957, 957, 958, 958, 959, 959, 960, 960, 961, 961, 962, 962 - 971, 971, 972, 972, 973, 973, 974, 974, 975, 975, 976, 976 - 979, 979, 980, 980, 981, 981 - 988, 988, 989, 989 - 994, 994, 995, 995 - 998, 998, 999, 999, 1000, 1000, 1001, 1001, 1002, 1002, 1003, 1003 - 1006, 1006, 1007, 1007 - 1016, 1016, 1017, 1017, 1018, 1018, 1019, 1019 - 1028, 1028, 1029, 1029 - 1034, 1034, 1035, 1035 - 1046, 1046, 1047, 1047 - 1058, 1058, 1059, 1059, 1060, 1060, 1061, 1061, 1062, 1062, 1063, 1063 - 1070, 1070, 1071, 1071, 1072, 1072, 1073, 1073, 1074, 1074, 1075, 1075 - 1078, 1078, 1079, 1079 - 1084, 1084, 1085, 1085, 1086, 1086, 1087, 1087 - 1092, 1092, 1093, 1093, 1094, 1094, 1095, 1095 - 1102, 1102, 1103, 1103 - 1114, 1114, 1115, 1115 - 1119, 1119, 1120, and SEQ ID NOS:1120 - 1124.

67. The use of any one of claims 62 or 63, wherein colorectal carcinoma is distinguished from at least one tissue selected from the group consisting of non-colon healthy tissue, peripheral blood lymphocytes and non-colon cancer tissue, and wherein the set of nucleic acids comprises at least two oligomers selected from one of the oligomer groups consisting of: SEQ ID NOS:59 - 109, 113 - 223, 227 - 293; and SEQ ID NOS:681 - 683, 683, 684, 684, 685, 685, 686, 686, 687, 687, 688, 688 - 691, 691, 692, 692 - 695, 695, 696, 696 - 699, 699, 700, 700 - 709, 709, 710, 710 - 725, 725, 726, 726, 727, 727, 728, 728 - 760, 760, 761, 761, 762, 762, 763, 763 - 777, 784, 784, 785, 785, 786, 786, 787, 787 - 802, 802, 803, 803 - 814, 814, 815, 815 - 832, 832, 833, 833 - 836, 836, 837, 837 - 872, 872, 873, 873 - 876, 876, 877, 877, 878, 878, 879, 879 - 882, 882, 883, 883 - 892, 892, 893, 893 - 896, 896, 897, 897 - 909, 909, 910, 910, 911, 911, 912, 912 - 915, 915, 916, 916 - 921, 921 - 925, 925, 926, 926 - 939, 939, 940, 940, 941, 941, 942, 942 - 944, 944 - 957, 957, 958, 958, 959, 959, 960, 960, 961, 961, 962, 962 - 971, 971, 972, 972, 973, 973, 974, 974, 975, 975, 976, 976 - 979, 979, 980, 980, 981, 981 - 988, 988, 989, 989 - 994, 994, 995, 995 - 998, 998, 999, 999, 1000, 1000, 1001, 1001, 1002, 1002, 1003, 1003, 1010 - 1016, 1016, 1017, 1017, 1018, 1018, 1019, 1019 - 1028, 1028, 1029, 1029 - 1034, 1034, 1035, 1035 - 1046, 1046, 1047, 1047 - 1058, 1058, 1059, 1059, 1060, 1060, 1061, 1061, 1062, 1062, 1063, 1063 - 1070, 1070, 1071, 1071, 1072, 1072, 1073, 1073, 1074, 1074, 1075, 1075 - 1078,

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68. The use of any one of claims 62 or 63, wherein colorectal carcinoma is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue, normal colon tissue, non-colon healthy tissue, peripheral blood lymphocytes, colon adenomas and non-colon cancer tissue, and wherein the set of nucleic acids comprises at least two oligomers selected from one of the oligomer groups consisting of: SEQ ID NOS:59 - 109, 113 - 161, 164 - 223, 227 - 285, 287 - 293; and SEQ ID NOS:681 - 683, 683, 684, 684, 685, 685, 686, 686, 687, 687, 688, 688 - 691, 691, 692, 692 - 695, 695, 696, 696 - 699, 699, 700, 700 - 709, 709, 710, 710 - 725, 725, 726, 726, 727, 727, 728, 728 - 760, 760, 761, 761, 762, 762, 763, 763 - 777, 784, 784, 785, 785, 786, 786, 787, 787 - 802, 802, 803, 803 - 814, 814, 815, 815 - 832, 832, 833, 833 - 836, 836, 837, 837 - 872, 872, 873, 873 - 876, 876, 877, 877, 878, 878, 879, 879 - 882, 882, 883, 883 - 885, 890 - 892, 892, 893, 893 - 896, 896, 897, 897 - 909, 909, 910, 910, 911, 911, 912, 912 - 915, 915, 916, 916 - 921, 921 - 925, 925, 926, 926 - 939, 939, 940, 940, 941, 941, 942, 942 - 944, 944 - 957, 957, 958, 958, 959, 959, 960, 960, 961, 961, 962, 962 - 971, 971, 972, 972, 973, 973, 974, 974, 975, 975, 976, 976 - 979, 979, 980, 980, 981, 981 - 988, 988, 989, 989 - 994, 994, 995, 995 - 998, 998, 999, 999, 1000, 1000, 1001, 1001, 1002, 1002, 1003, 1003, 1010 - 1016, 1016, 1017, 1017, 1018, 1018, 1019, 1019 - 1028, 1028, 1029, 1029 - 1034, 1034, 1035, 1035 - 1046, 1046, 1047, 1047 - 1058, 1058, 1059, 1059, 1060, 1060, 1061, 1061, 1062, 1062, 1063, 1063 - 1070, 1070, 1071, 1071, 1072, 1072, 1073, 1073, 1074, 1074, 1075, 1075 - 1078, 1078, 1079, 1079 - 1084, 1084, 1085, 1085, 1086, 1086, 1087, 1087 - 1092, 1092, 1093, 1093, 1094, 1094, 1095, 1095 - 1102, 1102, 1103, 1103 - 1114, 1114, 1115, 1115 - 1119, 1119, 1120, 1120 - 1124, 1129 - 1141, 1141, 1142, and SEQ ID NO:1142.

69. The use of any one of claims 62 or 63, wherein colorectal carcinoma is distinguished from colon adenomas, and wherein the set of nucleic acids comprises at least two

oligomers selected from one of the oligomer groups consisting of: SEQ ID NOS:89, 90, 126 - 135, 147 - 151, 224 - 226, 253 - 256, 261 - 267, 283 - 285; and SEQ ID NOS:738 - 740, 810 - 814, 814, 815, 815 - 829, 854 - 865, 1004 - 1006, 1006, 1007, 1007 - 1009, 1062, 1062, 1063, 1063 - 1069, 1078, 1078, 1079, 1079 - 1084, 1084, 1085, 1085, 1086, 1086, 1087, 1087 - 1091, and SEQ ID NOS:1121 - 1124.

70. The use of any one of claims 62 or 63, wherein at least one of colorectal carcinoma tissue, or colon adenomas is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue and normal colon tissue.
71. The use of one of claims 62 or 63, wherein colorectal carcinoma tissue is distinguished from at least one of inflammatory colon tissue and normal colon tissue, and wherein the set of nucleic acids comprises at least two oligomers selected from one of the oligomer groups consisting of: SEQ ID NOS:59 - 161, 164 - 293; and SEQ ID NOS:681 - 683, 683, 684, 684, 685, 685, 686, 686, 687, 687, 688, 688 - 691, 691, 692, 692 - 695, 695, 696, 696 - 699, 699, 700, 700 - 709, 709, 710, 710 - 725, 725, 726, 726, 727, 727, 728, 728 - 760, 760, 761, 761, 762, 762, 763, 763 - 784, 784, 785, 785, 786, 786, 787, 787 - 802, 802, 803, 803 - 814, 814, 815, 815 - 832, 832, 833, 833 - 836, 836, 837, 837 - 872, 872, 873, 873 - 876, 876, 877, 877, 878, 878, 879, 879 - 882, 882, 883, 883 - 885, 890 - 892, 892, 893, 893 - 896, 896, 897, 897 - 909, 909, 910, 910, 911, 911, 912, 912 - 915, 915, 916, 916 - 921, 921 - 925, 925, 926, 926 - 939, 939, 940, 940, 941, 941, 942, 942 - 944, 944 - 957, 957, 958, 958, 959, 959, 960, 960, 961, 961, 962, 962 - 971, 971, 972, 972, 973, 973, 974, 974, 975, 975, 976, 976 - 979, 979, 980, 980, 981, 981 - 988, 988, 989, 989 - 994, 994, 995, 995 - 998, 998, 999, 999, 1000, 1000, 1001, 1001, 1002, 1002, 1003, 1003 - 1006, 1006, 1007, 1007 - 1016, 1016, 1017, 1017, 1018, 1018, 1019, 1019 - 1028, 1028, 1029, 1029 - 1034, 1034, 1035, 1035 - 1046, 1046, 1047, 1047 - 1058, 1058, 1059, 1059, 1060, 1060, 1061, 1061, 1062, 1062, 1063, 1063 - 1070, 1070, 1071, 1071, 1072, 1072, 1073, 1073, 1074, 1074, 1075, 1075 - 1078, 1078, 1079, 1079 - 1084, 1084, 1085, 1085, 1086, 1086, 1087, 1087 - 1092, 1092, 1093, 1093, 1094, 1094, 1095, 1095 - 1102, 1102,

1103, 1103 - 1114, 1114, 1115, 1115 - 1119, 1119, 1120, 1120 - 1141, 1141, 1142, and SEQ ID NO:1142.

72. The use of one of claims 62 or 63, wherein at least one of colorectal carcinoma tissue, or colon adenomas is distinguished from at least one tissue selected from the group consisting of inflammatory colon tissue, normal colon tissue, non-colon healthy tissue, peripheral blood lymphocytes, and non-colon cancer tissue, and wherein the set of nucleic acids comprises at least two oligomers selected from one of the oligomer groups consisting of: SEQ ID NOS:59 - 109, 113 - 299; and SEQ ID NOS:681 - 683, 683, 684, 684, 685, 685, 686, 686, 687, 687, 688, 688 - 691, 691, 692, 692 - 695, 695, 696, 696 - 699, 699, 700, 700 - 709, 709, 710, 710 - 725, 725, 726, 726, 727, 727, 728, 728 - 760, 760, 761, 761, 762, 762, 763, 763 - 777, 784, 784, 785, 785, 786, 786, 787, 787 - 802, 802, 803, 803 - 814, 814, 815, 815 - 832, 832, 833, 833 - 836, 836, 837, 837 - 872, 872, 873, 873 - 876, 876, 877, 877, 878, 878, 879, 879 - 882, 882, 883, 883 - 892, 892, 893, 893 - 896, 896, 897, 897 - 909, 909, 910, 910, 911, 911, 912, 912 - 915, 915, 916, 916 - 921, 921 - 925, 925, 926, 926 - 939, 939, 940, 940, 941, 941, 942, 942 - 944, 944 - 957, 957, 958, 958, 959, 959, 960, 960, 961, 961, 962, 962 - 971, 971, 972, 972, 973, 973, 974, 974, 975, 975, 976, 976 - 979, 979, 980, 980, 981, 981 - 988, 988, 989, 989 - 994, 994, 995, 995 - 998, 998, 999, 999, 1000, 1000, 1001, 1001, 1002, 1002, 1003, 1003 - 1006, 1006, 1007, 1007 - 1016, 1016, 1017, 1017, 1018, 1018, 1019, 1019 - 1028, 1028, 1029, 1029 - 1034, 1034, 1035, 1035 - 1046, 1046, 1047, 1047 - 1058, 1058, 1059, 1059, 1060, 1060, 1061, 1061, 1062, 1062, 1063, 1063 - 1070, 1070, 1071, 1071, 1072, 1072, 1073, 1073, 1074, 1074, 1075, 1075 - 1078, 1078, 1079, 1079 - 1084, 1084, 1085, 1085, 1086, 1086, 1087, 1087 - 1092, 1092, 1093, 1093, 1094, 1094, 1095, 1095 - 1102, 1102, 1103, 1103 - 1114, 1114, 1115, 1115 - 1119, 1119, 1120, 1120 - 1141, 1141, 1142, 1142 - 1145, 1145, 1146, 1146, 1147, 1147, 1148, 1148 - 1151, 1151, 1152, and SEQ ID NO:1152.
73. The use of any one of claims 62 or 63, wherein tissues originating from the colon are distinguished from tissues of non-colon origin.

74. The use of claim 63, wherein cell proliferative disorders are distinguished from healthy tissues, and wherein the set of nucleic acids comprises at least two oligomers selected from one of the oligomer groups consisting of: SEQ ID NOS:59 - 109, 113 - 293, 296 - 299; and SEQ ID NOS:681 - 683, 683, 684, 684, 685, 685, 686, 686, 687, 687, 688, 688 - 691, 691, 692, 692 - 695, 695, 696, 696 - 699, 699, 700, 700 - 709, 709, 710, 710 - 725, 725, 726, 726, 727, 727, 728, 728 - 760, 760, 761, 761, 762, 762, 763, 763 - 777, 784, 784, 785, 785, 786, 786, 787, 787 - 802, 802, 803, 803 - 814, 814, 815, 815 - 832, 832, 833, 833 - 836, 836, 837, 837 - 872, 872, 873, 873 - 876, 876, 877, 877, 878, 878, 879, 879 - 882, 882, 883, 883 - 892, 892, 893, 893 - 896, 896, 897, 897 - 909, 909, 910, 910, 911, 911, 912, 912 - 915, 915, 916, 916 - 921, 921 - 925, 925, 926, 926 - 939, 939, 940, 940, 941, 941, 942, 942 - 944, 944 - 957, 957, 958, 958, 959, 959, 960, 960, 961, 961, 962, 962 - 971, 971, 972, 972, 973, 973, 974, 974, 975, 975, 976, 976 - 979, 979, 980, 980, 981, 981 - 988, 988, 989, 989 - 994, 994, 995, 995 - 998, 998, 999, 999, 1000, 1000, 1001, 1001, 1002, 1002, 1003, 1003 - 1006, 1006, 1007, 1007 - 1016, 1016, 1017, 1017, 1018, 1018, 1019, 1019 - 1028, 1028, 1029, 1029 - 1034, 1034, 1035, 1035 - 1046, 1046, 1047, 1047 - 1058, 1058, 1059, 1059, 1060, 1060, 1061, 1061, 1062, 1062, 1063, 1063 - 1070, 1070, 1071, 1071, 1072, 1072, 1073, 1073, 1074, 1074, 1075, 1075 - 1078, 1078, 1079, 1079 - 1084, 1084, 1085, 1085, 1086, 1086, 1087, 1087 - 1092, 1092, 1093, 1093, 1094, 1094, 1095, 1095 - 1102, 1102, 1103, 1103 - 1114, 1114, 1115, 1115 - 1119, 1119, 1120, 1120 - 1141, 1141, 1142, 1142, 1145, 1145, 1146, 1146, 1147, 1147, 1148, 1148 - 1151, 1151, 1152, and SEQ ID NO:1152.
75. Use of a set of oligomers according, in each case, to any one of Claims 56 through 61, as probes for determining at least one of a cytosine methylation state, or a single nucleotide polymorphism (SNP) of a sequence selected from the group consisting of SEQ ID NOS:1-58, and sequences complementary thereto.
76. The use of claim 63, wherein at least two oligomers according to any one of claims 56, 57 or 58, are used as primer oligonucleotides for the amplification of a DNA sequence

- of at least 16 contiguous nucleotides selected from the group consisting of SEQ ID NOS:304 to SEQ ID NO:535, and sequences complementary thereto.
77. Use of a nucleic acid according to Claim 57 for determination of at least one of cytosine methylation status of a corresponding genomic DNA, or detection of a single nucleotide polymorphism (SNP).
 78. The set of oligomers or isolated nucleic acids of any one of claims 59 or 60, wherein at least one oligomer selected from the group consisting of SEQ ID NOS:59 - 303 and SEQ ID NOS:681 to SEQ ID NO:1159 is bound to a solid phase.
 79. A method for manufacturing a nucleic acid array, comprising at least one of attachment of an oligomer according to any one of claims 56 through 58, or attachment of a set of oligomers or nucleic acids according to any one of claims 59 through 61, to a solid phase.
 80. An oligomer array manufactured according to Claim 79.
 81. The oligomer array of Claim 78, wherein the oligomers are bound to a planar solid phase in the form of a lattice selected from the group consisting of linear or substantially linear lattice, hexagonal or substantially hexagonal lattice, rectangular or substantially rectangular lattice, and lattice combinations thereof. Use of the oligomer array of claim 78 for the analysis of colon cell proliferative disorders.
 82. The array of claim 78, wherein the solid phase surface comprises a material selected from the group consisting of silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, gold, and combinations thereof.
 83. A kit useful for detecting, or for detecting distinguishing between or among colon cell proliferative disorders of a subject, comprising:
at least one of a bisulfite reagent, or a methylation-sensitive restriction enzyme; and at least one nucleic acid molecule or peptide nucleic acid molecule comprising, in each case a contiguous sequence at least 9 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID 304 to SEQ ID NO 535, and complements thereof.

84. The kit of claim 84, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethyLight, HeavyMethyl, COBRA, nucleic acid sequencing, and combinations thereof.
85. The method of any one of claims 1, 13 or 23, comprising use of the kit according to claim 84.
86. Use of a nucleic acid according to claims 52 through 55, an oligomer according to any one of claims 56 through 58, a set of oligonucleotides according to any one of claims 59 through 61, 64 and 65, a method of manufacturing according to claim 79, an array according to any one of claims 78, 80, 81 and 83 and a kit according to claim 84 for the detection of, detection and differentiation between or among subclasses of, diagnosis of, prognosis of, treatment of, monitoring of, or treatment and monitoring of colon cell proliferative disorders.